SEQUENCE LISTING

<110> Yissum Research Development Company of the Hebrew University of Jerusalem
Ben-Gurion University of the Negev Research and Development Authority
MANDELBOIM, Ofer
PORGADOR, Angel

<120> PEPTIDES DERIVED FROM NATURAL CYTOTOXICITY RECEPTORS AND METHODS OF USE THEREOF

<130> NAP/003/PCT

<140> PCT/IL2004
<141> 2004-11-24

<150> US 60/524,648
<151> 2003-11-25

<160> 30

<170> PatentIn version 3.3

<210> 1
<211> 23
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(23)
<223> amino acid residues 153-175 of human NKp46

<400> 1

Phe Leu Leu Leu Lys Glu Gly Arg Ser Ser His Val Gln Arg Gly Tyr
1 5 10 15

Gly Lys Val Gln Ala Glu Phe
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<210> 2
<211> 20
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<213> homo sapiens

<220>
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<222> (1)..(20)
<223> aa 153-172 of NKp46 (SEQ ID NO:5 herein)

<220>
<221> PEPTIDE
<222> (1)..(20)
<223> aa residues 153-172 of human NKp46 (SEQ ID NO:5 herein)

<400> 2

Phe Leu Leu Leu Lys Glu Gly Arg Ser Ser His Val Gln Arg Gly Tyr
1 5 10 15

Gly Lys Val Gln

20

<210> 3
<211> 28
<212> PRT
<213> homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> derived from NKp30 amino acids 56-83

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> amino acid residues 57-84 derived from human NKp30

<400> 3

Arg Asp Glu Val Val Pro Gly Lys Glu Val Arg Asn Gly Thr Pro Glu
1 5 10 15

Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser Ser Arg
20 25

<210> 4
<211> 20
<212> PRT
<213> homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(20)
<223> corresponds to amino acids 56-75 of NKp30

<220>
<221> PEPTIDE
<222> (1)..(20)
<223> amino acids residues 57-76 of human NKp30

<400> 4

Arg Asp Glu Val Val Pro Gly Lys Glu Val Arg Asn Gly Thr Pro Glu
1 5 10 15

Phe Arg Gly Arg
20

<210> 5
<211> 24
<212> PRT
<213> homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> amino acids 61-80 of NKp44

<220>
<221> PEPTIDE

<222> (1)..(24)
<223> amino acid residues 51-74 of human NKp44

<400> 5

Lys Lys Gly Trp Cys Lys Glu Ala Ser Ala Leu Val Cys Ile Arg Leu
1 5 10 15

Val Thr Ser Ser Lys Pro Arg Thr
20

<210> 6
<211> 304
<212> PRT
<213> homo sapiens

<300>
<308> NCBI/CAA04714
<309> 1998-09-22
<313> (1)..(304)

<400> 6

Met Ser Ser Thr Leu Pro Ala Leu Leu Cys Val Gly Leu Cys Leu Ser
1 5 10 15

Gln Arg Ile Ser Ala Gln Gln Gln Thr Leu Pro Lys Pro Phe Ile Trp
20 25 30

Ala Glu Pro His Phe Met Val Pro Lys Glu Lys Gln Val Thr Ile Cys
35 40 45

Cys Gln Gly Asn Tyr Gly Ala Val Glu Tyr Gln Leu His Phe Glu Gly
50 55 60

Ser Leu Phe Ala Val Asp Arg Pro Lys Pro Pro Glu Arg Ile Asn Lys
65 70 75 80

Val Lys Phe Tyr Ile Pro Asp Met Asn Ser Arg Met Ala Gly Gln Tyr
85 90 95

Ser Cys Ile Tyr Arg Val Gly Glu Leu Trp Ser Glu Pro Ser Asn Leu
100 105 110

Leu Asp Leu Val Val Thr Glu Met Tyr Asp Thr Pro Thr Leu Ser Val
115 120 125

His Pro Gly Pro Glu Val Ile Ser Gly Glu Lys Val Thr Phe Tyr Cys
130 135 140

Arg Leu Asp Thr Ala Thr Ser Met Phe Leu Leu Leu Lys Glu Gly Arg
145 150 155 160

Ser Ser His Val Gln Arg Gly Tyr Gly Lys Val Gln Ala Glu Phe Pro
165 170 175

Leu Gly Pro Val Thr Thr Ala His Arg Gly Thr Tyr Arg Cys Phe Gly
180 185 190

Ser Tyr Asn Asn His Ala Trp Ser Phe Pro Ser Glu Pro Val Lys Leu
195 200 205

Leu Val Thr Gly Asp Ile Glu Asn Thr Ser Leu Ala Pro Glu Asp Pro
210 215 220

Thr Phe Pro Ala Asp Thr Trp Gly Thr Tyr Leu Leu Thr Thr Glu Thr
225 230 235 240

Gly Leu Gln Lys Asp His Ala Leu Trp Asp His Thr Ala Gln Asn Leu
245 250 255

Leu Arg Met Gly Leu Ala Phe Leu Val Leu Val Ala Leu Val Trp Phe
260 265 270

Leu Val Glu Asp Trp Leu Ser Arg Lys Arg Thr Arg Glu Arg Ala Ser
275 280 285

Arg Ala Ser Thr Trp Glu Gly Arg Arg Arg Leu Asn Thr Gln Thr Leu
290 295 300

<210> 7
<211> 287
<212> PRT
<213> homo sapiens

<300>
<308> NCBI/CAA06872
<309> 1998-09-22
<313> (1)..(287)

<400> 7

Met Ser Ser Thr Leu Pro Ala Leu Leu Cys Val Gly Leu Cys Leu Ser
1 5 10 15

Gln Arg Ile Ser Ala Gln Gln Gln Thr Leu Pro Lys Pro Phe Ile Trp
20 25 30

Ala Glu Pro His Phe Met Val Pro Lys Glu Lys Gln Val Thr Ile Cys
35 40 45

Cys Gln Gly Asn Tyr Gly Ala Val Glu Tyr Gln Leu His Phe Glu Gly
50 55 60

Ser Leu Phe Ala Val Asp Arg Pro Lys Pro Pro Glu Arg Ile Asn Lys
65 70 75 80

Val Lys Phe Tyr Ile Pro Asp Met Asn Ser Arg Met Ala Gly Gln Tyr
85 90 95

```
Ser Cys Ile Tyr Arg Val Gly Glu Leu Trp Ser Glu Pro Ser Asn Leu
            100                 105                 110

Leu Asp Leu Val Val Thr Glu Met Tyr Asp Thr Pro Thr Leu Ser Val
        115                 120                 125

His Pro Gly Pro Glu Val Ile Ser Gly Glu Lys Val Thr Phe Tyr Cys
    130                 135                 140

Arg Leu Asp Thr Ala Thr Ser Met Phe Leu Leu Leu Lys Glu Gly Arg
145                 150                 155                 160

Ser Ser His Val Gln Arg Gly Tyr Gly Lys Val Gln Ala Glu Phe Pro
                165                 170                 175

Leu Gly Pro Val Thr Thr Ala His Arg Gly Thr Tyr Arg Cys Phe Gly
            180                 185                 190

Ser Tyr Asn Asn His Ala Trp Ser Phe Pro Ser Glu Pro Val Lys Leu
        195                 200                 205

Leu Val Thr Gly Asp Ile Glu Asn Thr Ser Leu Ala Pro Glu Asp Pro
    210                 215                 220

Thr Phe Pro Asp His Ala Leu Trp Asp His Thr Ala Gln Asn Leu Leu
225                 230                 235                 240

Arg Met Gly Leu Ala Phe Leu Val Leu Val Ala Leu Val Trp Phe Leu
                245                 250                 255

Val Glu Asp Trp Leu Ser Arg Lys Arg Thr Arg Glu Arg Ala Ser Arg
            260                 265                 270

Ala Ser Thr Trp Glu Gly Arg Arg Arg Leu Asn Thr Gln Thr Leu
        275                 280                 285
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<210> 8
<211> 209
<212> PRT
<213> homo sapiens

<300>
<308> NCBI/CAA06873
<309> 1998-09-22
<313> (1)..(209)

<400> 8

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Met Ser Ser Thr Leu Pro Ala Leu Leu Cys Val Gly Leu Cys Leu Ser
1               5                   10                  15

Gln Arg Ile Ser Ala Gln Gln Gln Met Tyr Asp Thr Pro Thr Leu Ser
            20                  25                  30
```

```
Val His Pro Gly Pro Glu Val Ile Ser Gly Glu Lys Val Thr Phe Tyr
        35                  40                  45

Cys Arg Leu Asp Thr Ala Thr Ser Met Phe Leu Leu Leu Lys Glu Gly
    50                  55                  60

Arg Ser Ser His Val Gln Arg Gly Tyr Gly Lys Val Gln Ala Glu Phe
65                  70                  75                  80

Pro Leu Gly Pro Val Thr Thr Ala His Arg Gly Thr Tyr Arg Cys Phe
                85                  90                  95

Gly Ser Tyr Asn Asn His Ala Trp Ser Phe Pro Ser Glu Pro Val Lys
            100                 105                 110

Leu Leu Val Thr Gly Asp Ile Glu Asn Thr Ser Leu Ala Pro Glu Asp
        115                 120                 125

Pro Thr Phe Pro Ala Asp Thr Trp Gly Thr Tyr Leu Leu Thr Thr Glu
    130                 135                 140

Thr Gly Leu Gln Lys Asp His Ala Leu Trp Asp His Thr Ala Gln Asn
145                 150                 155                 160

Leu Leu Arg Met Gly Leu Ala Phe Leu Val Leu Val Ala Leu Val Trp
                165                 170                 175

Phe Leu Val Glu Asp Trp Leu Ser Arg Lys Arg Thr Arg Glu Arg Ala
            180                 185                 190

Ser Arg Ala Ser Thr Trp Glu Gly Arg Arg Arg Leu Asn Thr Gln Thr
        195                 200                 205

Leu
```

<210> 9
<211> 192
<212> PRT
<213> homo sapiens

<300>
<308> NCBI/CAA06874
<309> 1998-09-22
<313> (1)..(192)

<400> 9

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Met Ser Ser Thr Leu Pro Ala Leu Leu Cys Val Gly Leu Cys Leu Ser
1               5                   10                  15

Gln Arg Ile Ser Ala Gln Gln Gln Met Tyr Asp Thr Pro Thr Leu Ser
            20                  25                  30
```

Val His Pro Gly Pro Glu Val Ile Ser Gly Glu Lys Val Thr Phe Tyr
35 40 45

Cys Arg Leu Asp Thr Ala Thr Ser Met Phe Leu Leu Leu Lys Glu Gly
50 55 60

Arg Ser Ser His Val Gln Arg Gly Tyr Gly Lys Val Gln Ala Glu Phe
65 70 75 80

Pro Leu Gly Pro Val Thr Thr Ala His Arg Gly Thr Tyr Arg Cys Phe
85 90 95

Gly Ser Tyr Asn Asn His Ala Trp Ser Phe Pro Ser Glu Pro Val Lys
100 105 110

Leu Leu Val Thr Gly Asp Ile Glu Asn Thr Ser Leu Ala Pro Glu Asp
115 120 125

Pro Thr Phe Pro Asp His Ala Leu Trp Asp His Thr Ala Gln Asn Leu
130 135 140

Leu Arg Met Gly Leu Ala Phe Leu Val Leu Val Ala Leu Val Trp Phe
145 150 155 160

Leu Val Glu Asp Trp Leu Ser Arg Lys Arg Thr Arg Glu Arg Ala Ser
165 170 175

Arg Ala Ser Thr Trp Glu Gly Arg Arg Arg Leu Asn Thr Gln Thr Leu
180 185 190

<210> 10
<211> 488
<212> PRT
<213> artificial

<220>
<223> conjugate of leader peptide, D1 and D2 domains of NKp46 with Fc domain

<400> 10

Met Ser Ser Thr Leu Pro Ala Leu Leu Cys Val Gly Leu Cys Leu Ser
1 5 10 15

Gln Arg Ile Ser Ala Gln Gln Gln Thr Leu Pro Lys Pro Phe Ile Trp
20 25 30

Ala Glu Pro His Phe Met Val Pro Lys Glu Lys Gln Val Thr Ile Cys
35 40 45

Cys Gln Gly Asn Tyr Gly Ala Val Glu Tyr Gln Leu His Phe Glu Gly
50 55 60

```
Ser Leu Phe Ala Val Asp Arg Pro Lys Pro Pro Glu Arg Ile Asn Lys
65                  70                  75                  80

Val Lys Phe Tyr Ile Pro Asp Met Asn Ser Arg Met Ala Gly Gln Tyr
                85                  90                  95

Ser Cys Ile Tyr Arg Val Gly Glu Leu Trp Ser Glu Pro Ser Asn Leu
            100                 105                 110

Leu Asp Leu Val Val Thr Glu Met Tyr Asp Thr Pro Thr Leu Ser Val
        115                 120                 125

His Pro Gly Pro Glu Val Ile Ser Gly Glu Lys Val Thr Phe Tyr Cys
    130                 135                 140

Arg Leu Asp Thr Ala Thr Ser Met Phe Leu Leu Leu Lys Glu Gly Arg
145                 150                 155                 160

Ser Ser His Val Gln Arg Gly Tyr Gly Lys Val Gln Ala Glu Phe Pro
                165                 170                 175

Leu Gly Pro Val Thr Thr Ala His Arg Gly Thr Tyr Arg Cys Phe Gly
            180                 185                 190

Ser Tyr Asn Asn His Ala Trp Ser Phe Pro Ser Glu Pro Val Lys Leu
        195                 200                 205

Leu Val Thr Gly Asp Ile Glu Asn Thr Ser Leu Ala Pro Glu Asp Pro
    210                 215                 220

Thr Phe Pro Ala Asp Thr Trp Gly Thr Tyr Leu Leu Thr Thr Glu Thr
225                 230                 235                 240

Gly Leu Gln Lys Asp His Ala Leu Trp Asp His Thr Ala Gln Asp Pro
                245                 250                 255

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
            260                 265                 270

Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
        275                 280                 285

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
    290                 295                 300

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
305                 310                 315                 320

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
                325                 330                 335
```

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
340 345 350

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
355 360 365

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
370 375 380

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
385 390 395 400

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
405 410 415

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
420 425 430

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
435 440 445

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
450 455 460

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
465 470 475 480

Ser Leu Ser Leu Ser Pro Gly Lys
485

<210> 11
<211> 364
<212> PRT
<213> artificial

<220>
<223> conjugate of CD5 leader peptide and D1 of NKp46 with Fc domain

<400> 11

Met Gly Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu
1 5 10 15

Leu Gly Met Leu Val Ala Ser Cys Leu Gly Arg Leu Arg Val Pro Gln
20 25 30

Gln Gln Thr Leu Pro Lys Pro Phe Ile Trp Ala Glu Pro His Phe Met
35 40 45

Val Pro Lys Glu Lys Gln Val Thr Ile Cys Cys Gln Gly Asn Tyr Gly
50 55 60

Ala Val Glu Tyr Gln Leu His Phe Glu Gly Ser Leu Phe Ala Val Asp
65 70 75 80

```
Arg Pro Lys Pro Pro Glu Arg Ile Asn Lys Val Lys Phe Tyr Ile Pro
                85                  90                  95

Asp Met Asn Ser Arg Met Ala Gly Gln Tyr Ser Cys Ile Tyr Arg Val
            100                 105                 110

Gly Glu Leu Trp Ser Glu Pro Ser Asn Leu Leu Asp Leu Val Val Thr
        115                 120                 125

Glu Met Asp Pro Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro
    130                 135                 140

Pro Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe
145                 150                 155                 160

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                165                 170                 175

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
            180                 185                 190

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        195                 200                 205

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    210                 215                 220

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
225                 230                 235                 240

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                245                 250                 255

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            260                 265                 270

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        275                 280                 285

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    290                 295                 300

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
305                 310                 315                 320

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                325                 330                 335

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            340                 345                 350
```

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
355 360

<210> 12
<211> 393
<212> PRT
<213> artificial

<220>
<223> conjugate of CD5 leader peptide and D2 domain of NKp46 with Fc domain

<400> 12

Met Gly Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu
1 5 10 15

Leu Gly Met Leu Val Ala Ser Cys Leu Gly Arg Leu Arg Val Pro Tyr
20 25 30

Asp Thr Pro Thr Leu Ser Val His Pro Gly Pro Glu Val Ile Ser Gly
35 40 45

Glu Lys Val Thr Phe Tyr Cys Arg Leu Asp Thr Ala Thr Ser Met Phe
50 55 60

Leu Leu Leu Lys Glu Gly Arg Ser Ser His Val Gln Arg Gly Tyr Gly
65 70 75 80

Lys Val Gln Ala Glu Phe Pro Leu Gly Pro Val Thr Thr Ala His Arg
85 90 95

Gly Thr Tyr Arg Cys Phe Gly Ser Tyr Asn Asn His Ala Trp Ser Phe
100 105 110

Pro Ser Glu Pro Val Lys Leu Leu Val Thr Gly Asp Ile Glu Asn Thr
115 120 125

Ser Leu Ala Pro Glu Asp Pro Thr Phe Pro Asp Thr Trp Gly Thr Tyr
130 135 140

Leu Leu Thr Thr Glu Thr Gly Leu Gln Lys Asp His Ala Leu Trp Asp
145 150 155 160

Pro Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
165 170 175

Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
180 185 190

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
195 200 205

```
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    210                 215                 220

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
225                 230                 235                 240

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                245                 250                 255

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            260                 265                 270

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        275                 280                 285

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    290                 295                 300

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
305                 310                 315                 320

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                325                 330                 335

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            340                 345                 350

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        355                 360                 365

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    370                 375                 380

Lys Ser Leu Ser Leu Ser Pro Gly Lys
385                 390
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<210> 13
<211> 201
<212> PRT
<213> homo sapiens

<300>
<308> NCBI/AAH52582
<309> 2004-06-30
<313> (1)..(201)

<400> 13

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Met Ala Trp Met Leu Leu Leu Ile Leu Ile Met Val His Pro Gly Ser
1               5                   10                  15

Cys Ala Leu Trp Val Ser Gln Pro Pro Glu Ile Arg Thr Leu Glu Gly
            20                  25                  30
```

Ser Ser Ala Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu
35 40 45

Ala Ile Gly Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys
50 55 60

Glu Val Arg Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu
65 70 75 80

Ala Ser Ser Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg
85 90 95

Asp Val Arg Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val
100 105 110

Leu Gly Leu Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu
115 120 125

Lys Glu His Pro Gln Leu Gly Ala Gly Thr Val Leu Leu Leu Arg Ala
130 135 140

Gly Phe Tyr Ala Val Ser Phe Leu Ser Val Ala Val Gly Ser Thr Val
145 150 155 160

Tyr Tyr Gln Gly Lys Cys Leu Thr Trp Lys Gly Pro Arg Arg Gln Leu
165 170 175

Pro Ala Val Val Pro Ala Pro Leu Pro Pro Pro Cys Gly Ser Ser Ala
180 185 190

His Leu Leu Pro Pro Val Pro Gly Gly
195 200

<210> 14
<211> 382
<212> PRT
<213> artificial

<220>
<223> conjugate of CD5 leader peptide and D (Ig-like )domain of NKp30 with Fc domain

<400> 14

Met Gly Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu
1 5 10 15

Leu Gly Met Leu Val Ala Ser Cys Leu Gly Arg Leu Arg Val Pro Leu
20 25 30

Trp Val Ser Gln Pro Leu Glu Ile Arg Thr Leu Glu Gly Ser Ser Ala
35 40 45

```
Phe Leu Pro Cys Ser Phe Asn Ala Ser Gln Gly Arg Leu Ala Ile Gly
    50                  55                  60

Ser Val Thr Trp Phe Arg Asp Glu Val Val Pro Gly Lys Glu Val Arg
65                  70                  75                  80

Asn Gly Thr Pro Glu Phe Arg Gly Arg Leu Ala Pro Leu Ala Ser Ser
                85                  90                  95

Arg Phe Leu His Asp His Gln Ala Glu Leu His Ile Arg Asp Val Arg
            100                 105                 110

Gly His Asp Ala Ser Ile Tyr Val Cys Arg Val Glu Val Leu Gly Leu
        115                 120                 125

Gly Val Gly Thr Gly Asn Gly Thr Arg Leu Val Val Glu Lys Glu His
    130                 135                 140

Pro Gln Leu Gly Asp Pro Glu Pro Lys Ser Ser Asp Lys Thr His Thr
145                 150                 155                 160

Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Ala Pro Ser Val Phe
                165                 170                 175

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            180                 185                 190

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
        195                 200                 205

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
    210                 215                 220

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
225                 230                 235                 240

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
                245                 250                 255

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            260                 265                 270

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
        275                 280                 285

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
    290                 295                 300

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
305                 310                 315                 320
```

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
325 330 335

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
340 345 350

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
355 360 365

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

<210> 15
<211> 276
<212> PRT
<213> homo sapiens

<300>
<308> NCBI/CAB39168
<309> 1999-03-15
<313> (1)..(276)

<400> 15

Met Ala Trp Arg Ala Leu His Pro Leu Leu Leu Leu Leu Leu Leu Phe
1 5 10 15

Pro Gly Ser Gln Ala Gln Ser Lys Ala Gln Val Leu Gln Ser Val Ala
20 25 30

Gly Gln Thr Leu Thr Val Arg Cys Gln Tyr Pro Pro Thr Gly Ser Leu
35 40 45

Tyr Glu Lys Lys Gly Trp Cys Lys Glu Ala Ser Ala Leu Val Cys Ile
50 55 60

Arg Leu Val Thr Ser Ser Lys Pro Arg Thr Met Ala Trp Thr Ser Arg
65 70 75 80

Phe Thr Ile Trp Asp Asp Pro Asp Ala Gly Phe Phe Thr Val Thr Met
85 90 95

Thr Asp Leu Arg Glu Glu Asp Ser Gly His Tyr Trp Cys Arg Ile Tyr
100 105 110

Arg Pro Ser Asp Asn Ser Val Ser Lys Ser Val Arg Phe Tyr Leu Val
115 120 125

Val Ser Pro Ala Ser Ala Ser Thr Gln Thr Pro Trp Thr Pro Arg Asp
130 135 140

Leu Val Ser Ser Gln Thr Gln Thr Gln Ser Cys Val Pro Pro Thr Ala
145 150 155 160

Gly Ala Arg Gln Ala Pro Glu Ser Pro Ser Thr Ile Pro Val Pro Ser
165 170 175

Gln Pro Gln Asn Ser Thr Leu Arg Pro Gly Pro Ala Ala Pro Ile Ala
180 185 190

Leu Val Pro Val Phe Cys Gly Leu Leu Val Ala Lys Ser Leu Val Leu
195 200 205

Ser Ala Leu Leu Val Trp Trp Gly Asp Ile Trp Trp Lys Thr Val Met
210 215 220

Glu Leu Arg Ser Leu Asp Thr Gln Lys Ala Thr Cys His Leu Gln Gln
225 230 235 240

Val Thr Asp Leu Pro Trp Thr Ser Val Ser Ser Pro Val Glu Arg Glu
245 250 255

Ile Leu Tyr His Thr Val Ala Arg Thr Lys Ile Ser Asp Asp Asp Asp
260 265 270

Glu His Thr Leu
275

<210> 16
<211> 434
<212> PRT
<213> artificial

<220>
<223> conjugate of leader peptide, DS and DL domains of NKp44 with Fc domain

<400> 16

Met Gly Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu
1 5 10 15

Leu Gly Met Leu Val Ala Ser Cys Leu Gly Arg Leu Arg Val Pro Gln
20 25 30

Ser Lys Ala Gln Val Leu Gln Ser Val Ala Gly Gln Thr Leu Thr Val
35 40 45

Arg Cys Gln Tyr Pro Pro Thr Gly Ser Leu Tyr Glu Lys Lys Gly Trp
50 55 60

Cys Lys Glu Ala Ser Ala Leu Val Cys Ile Arg Leu Val Thr Ser Ser
65 70 75 80

Lys Pro Arg Thr Val Ala Trp Thr Ser Arg Phe Thr Ile Trp Asp Asp
85 90 95

Pro Asp Ala Gly Phe Phe Thr Val Thr Met Thr Asp Leu Arg Glu Glu

100 105 110

Asp Ser Gly His Tyr Trp Cys Arg Ile Tyr Arg Pro Ser Asp Asn Ser
115 120 125

Val Ser Lys Ser Val Arg Phe Tyr Leu Val Val Ser Pro Ala Ser Ala
130 135 140

Ser Thr Gln Thr Ser Trp Thr Pro Arg Asp Leu Val Ser Ser Gln Thr
145 150 155 160

Gln Thr Gln Ser Cys Val Pro Pro Thr Ala Gly Ala Arg Gln Ala Pro
165 170 175

Glu Ser Pro Ser Thr Ile Pro Val Pro Ser Gln Pro Gln Asn Ser Thr
180 185 190

Leu Arg Pro Gly Pro Ala Ala Pro Asp Pro Glu Pro Lys Ser Ser Asp
195 200 205

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly Ala
210 215 220

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
225 230 235 240

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
245 250 255

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
260 265 270

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
275 280 285

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
290 295 300

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
305 310 315 320

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
325 330 335

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
340 345 350

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
355 360 365

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

370 375 380

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
385 390 395 400

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
405 410 415

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
420 425 430

Gly Lys

<210> 17
<211> 326
<212> PRT
<213> artificial

<220>
<223> conjugate of CD5 leader peptide and DS domain of NKP44 with Fc domain

<400> 17

Met Gly Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu
1 5 10 15

Leu Gly Met Leu Val Ala Ser Cys Leu Gly Arg Leu Arg Val Pro Ser
20 25 30

Pro Ala Ser Ala Ser Thr Gln Thr Ser Trp Thr Pro Arg Asp Leu Val
35 40 45

Ser Ser Gln Thr Gln Thr Gln Ser Cys Val Pro Pro Thr Ala Gly Ala
50 55 60

Arg Gln Ala Pro Glu Ser Pro Ser Thr Ile Pro Val Pro Ser Gln Pro
65 70 75 80

Gln Asn Ser Thr Leu Arg Pro Gly Pro Ala Ala Pro Asp Pro Glu Pro
85 90 95

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
100 105 110

Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
165 170 175

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
195 200 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 18
<211> 376
<212> PRT
<213> artificial

<220>
<223> conjugate of leader peptide,and DL domain of Nkp44 with Fc domain

<400> 18

Met Gly Met Pro Met Gly Ser Phe Gln Pro Leu Ala Thr Leu Tyr Leu
1 5 10 15

Leu Gly Met Leu Val Ala Ser Cys Leu Gly Arg Leu Arg Val Pro Gln
20 25 30

Ser Lys Ala Gln Val Leu Gln Ser Val Ala Gly Gln Thr Leu Thr Val
35 40 45

Arg Cys Gln Tyr Pro Pro Thr Gly Ser Leu Tyr Glu Lys Lys Gly Trp
50 55 60

Cys Lys Glu Ala Ser Ala Leu Val Cys Ile Arg Leu Val Thr Ser Ser
65 70 75 80

Lys Pro Arg Thr Val Ala Trp Thr Ser Arg Phe Thr Ile Trp Asp Asp
85 90 95

Pro Asp Ala Gly Phe Phe Thr Val Thr Met Thr Asp Leu Arg Glu Glu
100 105 110

Asp Ser Gly His Tyr Trp Cys Arg Ile Tyr Arg Pro Ser Asp Asn Ser
115 120 125

Val Ser Lys Ser Val Arg Phe Tyr Leu Val Val Ser Pro Ala Asp Pro
130 135 140

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
145 150 155 160

Pro Glu Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
165 170 175

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
180 185 190

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
195 200 205

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
210 215 220

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
225 230 235 240

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
245 250 255

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
260 265 270

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
275 280 285

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
290 295 300

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
305 310 315 320

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
325 330 335

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
340 345 350

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
355 360 365

Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 19
<211> 914
<212> DNA
<213> homo sapiens

<300>
<308> NCBI/AJ001383
<309> 1998-09-22
<313> (1)..(914)

<400> 19
tgtcttccac actccctgcc ctgctctgcg tcgggctgtg tctgagtcag aggatcagcg 60

cccagcagca gactctccca aaaccgttca tctgggccga gccccatttc atggttccaa 120

aggaaaagca agtgaccatc tgttgccagg gaaattatgg ggctgttgaa taccagctgc 180

actttgaagg aagccttttt gccgtggaca gaccaaaacc ccctgagcgg attaacaaag 240

tcaaattcta catcccggac atgaactccc gcatggcagg gcaatacagc tgcatctatc 300

gggttgggga gctctggtca gagcccagca acttgctgga tctggtggta acagaaatgt 360

atgacacacc caccctctcg gttcatcctg gacccgaagt gatctcggga gagaaggtga 420

ccttctactg ccgtctagac actgcaacaa gcatgttctt actgctcaag gagggaagat 480

ccagccacgt acagcgcgga tacgggaagg tccaggcgga gttccccctg ggccctgtga 540

ccacagccca ccgagggaca taccgatgtt ttggctccta taacaaccat gcctggtctt 600

tccccagtga gccagtgaag ctcctggtca caggcgacat tgagaacacc agccttgcac 660

ctgaagaccc caccttcct gcagacactt ggggcaccta ccttttaacc acagagacgg 720

gactccagaa agaccatgcc ctctgggatc acactgccca gaatctcctt cggatgggcc 780

tggcctttct agtcctggtg gctctagtgt ggttcctggt tgaagactgg ctcagcagga 840

agaggactag agagcgagcc agcagagctt ccacttggga aggcaggaga aggctgaaca 900

cacagactct ttga 914

<210> 20
<211> 1506
<212> DNA
<213> artificial

<220>
<223> DNA sequence of conjugate of leader peptide, D1 AND D2 domains of NKp46 with Fc domain (SEQ ID NO:9)

<400> 20
tccccactgc tcagcactta ggccggcaga atctgagcga tgtcttccac actccctgcc 60
ctgctctgcg tcgggctgtg tctgagtcag aggatcagcg cccagcagca gactctccca 120
aaaccgttca tctgggccga gccccatttc atggttccaa aggaaaagca agtgaccatc 180
tgttgccagg gaaattatgg ggctgttgaa taccagctgc actttgaagg aagccttttt 240
gccgtggaca gaccaaaacc ccctgagcgg attaacaaag tcaaattcta catcccggac 300
atgaactccc gcatggcagg gcaatacagc tgcatctatc gggttgggga gctctggtca 360
gagcccagca acttgctgga tctggtggta acagaaatgt atgacacacc caccctctcg 420
gttcatcctg gacccgaagt gatctcggga gagaaggtga ccttctactg ccgtctagac 480
actgcaacaa gcatgttctt actgctcaag gagggaagat ccagccacgt acagcgcgga 540
tacgggaagg tccaggcgga gttccccctg ggccctgtga ccacagccca ccgagggaca 600
taccgatgtt ttggctccta taacaaccat gcctggtctt tccccagtga gccagtgaag 660
ctcctggtca caggcgacat tgagaacacc agccttgcac ctgaagaccc caccttcct 720
gcagacactt ggggcaccta ccttttaacc acagagacgg gactccagaa agaccatgcc 780
ctctgggatc acactgccca ggatccggag cccaaatctt ctgacaaaac tcacacatgc 840
ccaccgtgcc cagcacctga attcgagggt gcaccgtcag tcttcctctt ccccccaaaa 900
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 960
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 1020
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 1080
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 1140
gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 1200
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 1260
tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 1320
ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 1380
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1440
gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1500
aaatga 1506

<210> 21
<211> 1110
<212> DNA
<213> artificial

<220>
<223> DNA encoding conjugate of CD5 leader peptideand D1 domain of NKP46 with Fc domain (SEQ ID NO:10)

<400> 21
aagcttgccg ccaccatggg aatgcccatg gggtctctgc aaccgctggc caccttgtac 60
ctgctgggga tgctggtcgc ttcctgcctc ggacggctca gggtacccca gcagcagact 120

ctcccaaaac cgttcatctg ggccgagccc catttcatgg ttccaaagga aaagcaagtg 180
accatctgtt gccagggaaa ttatggggct gttgaatacc agctgcactt tgaaggaagc 240
ctttttgccg tggacagacc aaaaccccct gagcggatta acaaagtcaa attctacatc 300
ccggacatga actcccgcat ggcagggcaa tacagctgca tctatcgggt tggggagctc 360
tggtcagagc ccagcaactt gctggatctg gtggtaacag aaatggatcc ggagcccaaa 420
tcttctgaca aaactcacac atgcccaccg tgcccagcac ctgaattcga gggtgcaccg 480
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 540
gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 600
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 660
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 720
tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 780
gccaaagggc agccccgaga gccacaggtg tacaccctgc ccccatcccg ggatgagctg 840
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 900
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 960
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1020
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1080
aagagcctct ccctgtctcc gggtaaatga 1110

<210> 22
<211> 1197
<212> DNA
<213> artificial

<220>
<223> DNA encoding conjugate of leader peptide and D2 domain of NKP46 with Fc domain (SEQ ID NO:12)

<400> 22
aagcttgccg ccaccatggg aatgcccatg gggtctctgc aaccgctggc caccttgtac 60
ctgctgggga tgctggtcgc ttcctgcctc ggacggctca gggtacccta tgacacaccc 120
accctctcgg ttcatcctgg acccgaggtg atctcgggag agaaggtgac cttctactgc 180
cgtctagaca ctgcaacaag catgttctta ctgctcaagg agggaagatc cagccacgta 240
cagcgcggat acgggaaggt ccaggcggag ttccccctgg gccctgtgac cacagcccac 300
cgagggacat accgatgttt tggctcctat aacaaccatg cctggtcttt ccccagtgag 360
ccagtgaagc tcctggtcac aggcgacatt gagaacacca gccttgcacc tgaagacccc 420
acctttcctg acacttgggg cacctacctt ttaaccacag agacgggact ccagaaagac 480
catgccctct gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc 540
ccagcacctg aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac 600
accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 660

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 720

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 780

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 840

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagagcc acaggtgtac 900

accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 960

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1020

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1080

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1140

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatga 1197

<210> 23
<211> 606
<212> DNA
<213> homo sapiens

<300>
<308> NCBI/BC052582
<309> 2004-06-30
<313> (1)..(606)

<400> 23
atggcctgga tgctgttgct catcttgatc atggtccatc caggatcctg tgctctctgg 60

gtgtcccagc cccctgagat tcgtaccctg gaaggatcct ctgccttcct gccctgctcc 120

ttcaatgcca gccaagggag actggccatt ggctccgtca cgtggttccg agatgaggtg 180

gttccaggga aggaggtgag gaatggaacc ccagagttca ggggccgcct ggccccactt 240

gcttcttccc gtttcctcca tgaccaccag gctgagctgc acatccggga cgtgcgaggc 300

catgacgcca gcatctacgt gtgcagagtg gaggtgctgg gccttggtgt cgggacaggg 360

aatgggactc ggctggtggt ggagaaagaa catcctcagc taggggctgg tacagtcctc 420

ctccttcggg ctggattcta tgctgtcagc tttctctctg tggccgtggg cagcaccgtc 480

tattaccagg gcaaatgtct gacctggaaa ggtccaagaa ggcagctgcc ggctgtggtc 540

ccagcgcccc tcccaccacc atgtgggagc tcagcacatc tgcttccccc agtcccagga 600

ggctga 606

<210> 24
<211> 1164
<212> DNA
<213> artificial

<220>
<223> DNA encoding conjugate of CD5 leader peptide, D1 and D2 domains of NKp30 with Fc domain (SEQ ID NO:13)

<400> 24
aagcttgccg ccaccatggg aatgcccatg gggtctctgc aaccgctggc caccttgtac 60

ctgctgggga tgctggtcgc ttcctgcctc ggacggctca gggtacccct ctgggtgtcc 120

cagccccttg agattcgtac cctggaaggg tcttctgcct tcctgccctg ctccttcaat 180

gccagccaag ggagactggc cattggctcc gtcacgtggt tccgagatga ggtggttcca 240
gggaaggagg tgaggaatgg aaccccagag ttcaggggcc gcctggcccc acttgcttct 300
tcccgtttcc tccatgacca ccaggctgag ctgcacatcc gggacgtgcg aggccatgac 360
gccagcatct acgtgtgcag agtggaggtg ctgggccttg gtgtcgggac agggaatggg 420
actcggctgg tggtggagaa agaacatcct cagctagggg atccggagcc caaatcttct 480
gacaaaactc acacatgccc accgtgccca gcacctgaat tcgagggtgc accgtcagtc 540
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 600
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 660
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 720
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 780
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 840
gggcagcccc gagagccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 900
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 960
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1020
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1080
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1140
ctctccctgt ctccgggtaa atga 1164

<210> 25
<211> 854
<212> DNA
<213> homo sapiens

<300>
<308> NCBI/AJ225109
<309> 1999-03-15
<313> (1)..(854)

<400> 25
atggcctggc gagccctaca cccactgcta ctgctgctgc tgctgttccc aggctctcag 60
gcacaatcca aggctcaggt acttcaaagt gtggcagggc agacgctaac cgtgagatgc 120
cagtacccgc ccacgggcag tctctacgag aagaaaggct ggtgtaagga ggcttcagca 180
cttgtgtgca tcaggttagt caccagctcc aagcccagga cgatggcttg gacctctcga 240
ttcacaatct gggacgaccc tgatgctggc ttcttcactg tcaccatgac tgatctgaga 300
gaggaagact caggacatta ctggtgtaga atctaccgcc cttctgacaa ctctgtctct 360
aagtccgtca gattctatct ggtggtatct ccagcctctg cctccacaca gacccctgg 420
actccccgcg acctggtctc ttcacagacc cagacccaga gctgtgtgcc tcccactgca 480
ggagccagac aagcccctga gtctccatct accatccctg tcccttcaca gccacagaac 540
tccacgctcc gccctggccc tgcagccccc attgccctgg tgcctgtgtt ctgtggactc 600
ctcgtagcca agagcctggt gctgtcagcc ctgctcgtct ggtgggggga catatggtgg 660

aaaaccgtga tggagctcag gagcctggat acccaaaaag ccacctgcca ccttcaacag 720

gtcacggacc ttccctggac ctcagtttcc tcacctgtag agagagaaat attatatcac 780

actgttgcaa ggactaagat aagcgatgat gatgatgaac acactttgtg aataataaaa 840

ttatctgaat gttt 854

<210> 26
<211> 1320
<212> DNA
<213> artificial

<220>
<223> DNA encoding conjugate of leader peptide, DS and DL domains of NKp44 with Fc domain (SEQ ID NO:15)

<400> 26
aagcttgccg ccaccatggg aatgcccatg gggtctctgc aaccgctggc caccttgtac 60

ctgctgggga tgctggtcgc ttcctgcctc ggacggctca gggtacccca atccaaggct 120

caggtacttc aaagtgtggc agggcagacg ctaaccgtga gatgccagta cccgcccacg 180

ggcagtctct acgagaagaa aggctggtgt aaggaggctt cagcacttgt gtgcatcagg 240

ttagtcacca gctccaagcc caggacggtg gcttggacct ctcgattcac aatctgggac 300

gaccctgatg ctggcttctt cactgtcacc atgactgatc tgagagagga agactcagga 360

cattactggt gtagaatcta ccgcccttct gacaactctg tctctaagtc cgtcagattc 420

tatctggtgg tatctccagc ctctgcctcc acacagacct cctggactcc ccgcgacctg 480

gtctcttcac agacccagac ccagagctgt gtgcctccca ctgcaggagc cagacaagcc 540

cctgagtctc catctaccat ccctgtccct tcacagccac agaactccac gctccgccct 600

ggccctgcag ccccggatcc ggagcccaaa tcttctgaca aaactcacac atgcccaccg 660

tgcccagcac ctgaattcga gggtgcaccg tcagtcttcc tcttcccccc aaaacccaag 720

gacaccctca tgatctcccg gaccctgag gtcacatgcg tggtggtgga cgtgagccac 780

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag 840

acaaagccgc gggaggagca gtacaacagc acgtaccgtg tggtcagcgt cctcaccgtc 900

ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc 960

ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga gccacaggtg 1020

tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg 1080

gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1140

aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc 1200

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1260

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatga 1320

<210> 27
<211> 996
<212> DNA

<213> artificial

<220>
<223> DNA encoding conjugate of CD5 leader peptide and DS domain of NKp44 with Fc domain (SEQ ID NO:16)

<400> 27
aagcttgccg ccaccatggg aatgcccatg gggtctctgc aaccgctggc caccttgtac 60
ctgctgggga tgctggtcgc ttcctgcctc ggacggctca gggtaccctc tccagcctct 120
gcctccacac agacctcctg gactccccgc gacctggtct cttcacagac ccagacccag 180
agctgtgtgc ctcccactgc aggagccaga caagcccctg agtctccatc taccatccct 240
gtcccttcac agccacagaa ctccacgctc cgccctggcc ctgcagcccc ggatccggag 300
cccaaatctt ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga attcgagggt 360
gcaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 420
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 480
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 540
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 600
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccccatcga gaaaaccatc 660
tccaaagcca aagggcagcc ccgagagcca caggtgtaca ccctgccccc atcccgggat 720
gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 780
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 840
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 900
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 960
acgcagaaga gcctctccct gtctccgggt aaatga 996

<210> 28
<211> 1146
<212> DNA
<213> artificial

<220>
<223> DNA encoding conjugate of CD5 leader peptide and DL domain of NKp44 with Fc domain (SEQ ID NO:17)

<400> 28
aagcttgccg ccaccatggg aatgcccatg gggtctctgc aaccgctggc caccttgtac 60
ctgctgggga tgctggtcgc ttcctgcctc ggacggctca gggtacccca atccaaggct 120
caggtacttc aaagtgtggc agggcagacg ctaaccgtga gatgccagta cccgcccacg 180
ggcagtctct acgagaagaa aggctggtgt aaggaggctt cagcacttgt gtgcatcagg 240
ttagtcacca gctccaagcc caggacggtg gcttggacct ctcgattcac aatctgggac 300
gaccctgatg ctggcttctt cactgtcacc atgactgatc tgagagagga agactcagga 360
cattactggt gtagaatcta ccgcccttct gacaactctg tctctaagtc cgtcagattc 420
tatctggtgg tatctccagc ggatccggag cccaaatctt ctgacaaaac tcacacatgc 480

ccaccgtgcc cagcacctga attcgagggt gcaccgtcag tcttcctctt ccccccaaaa 540
cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 600
agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 660
gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 720
accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 780
gccctcccag cccccatcga gaaaaccatc tccaaagcca aagggcagcc ccgagagcca 840
caggtgtaca ccctgccccc atcccgggat gagctgacca agaaccaggt cagcctgacc 900
tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 960
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Asp Thr Pro Thr Leu Ser Val His Pro Gly Pro Glu Val Ile Ser Gly
35 40 45

Glu Lys Val Thr Phe Tyr Cys Arg Leu Asp Thr Ala Thr Ser Met Phe
50 55 60

Leu Leu Leu Gln Glu Gly Gln Ser Ser Gln Val Gln Gln Gly Tyr Gly
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Lys Val Gln Ala Glu Phe Pro Leu Gly Pro Val Thr Thr Ala His Arg
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Gly Thr Tyr Arg Cys Phe Gly Ser Tyr Asn Asn His Ala Trp Ser Phe
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Pro Ser Glu Pro Val Lys Leu Leu Val Thr Gly Asp Ile Glu Asn Thr
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Leu Leu Thr Thr Glu Thr Gly Leu Gln Lys Asp His Ala Leu Trp
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35 40 45

Glu Lys Val Thr Phe Tyr Cys Arg Leu Asp Thr Ala Thr Ser Met Phe
50 55 60

Leu Leu Leu Gln Glu Gly Gln Ser Ser Gln Val Gln Gln Gly Tyr Gly
65 70 75 80

Thr Val Gln Ala Glu Phe Pro Leu Gly Pro Val Thr Thr Ala His Arg
85 90 95

Gly Thr Tyr Arg Cys Phe Gly Ser Tyr Asn Asn His Ala Trp Ser Phe
100 105 110

Pro Ser Glu Pro Val Lys Leu Leu Val Thr Gly Asp Ile Glu Asn Thr
115 120 125

Ser Leu Ala Pro Glu Asp Pro Thr Phe Pro Asp Thr Trp Gly Thr Tyr
130 135 140

Leu Leu Thr Thr Glu Thr Gly Leu Gln Lys Asp His Ala Leu Trp
145 150 155